

results of **BLAST**

CD

BLASTP 2.2.6 [Apr-09-2003]**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1054225001-026414-17909

Query=

(23 letters)

Database: All non-redundant GenBank CDS

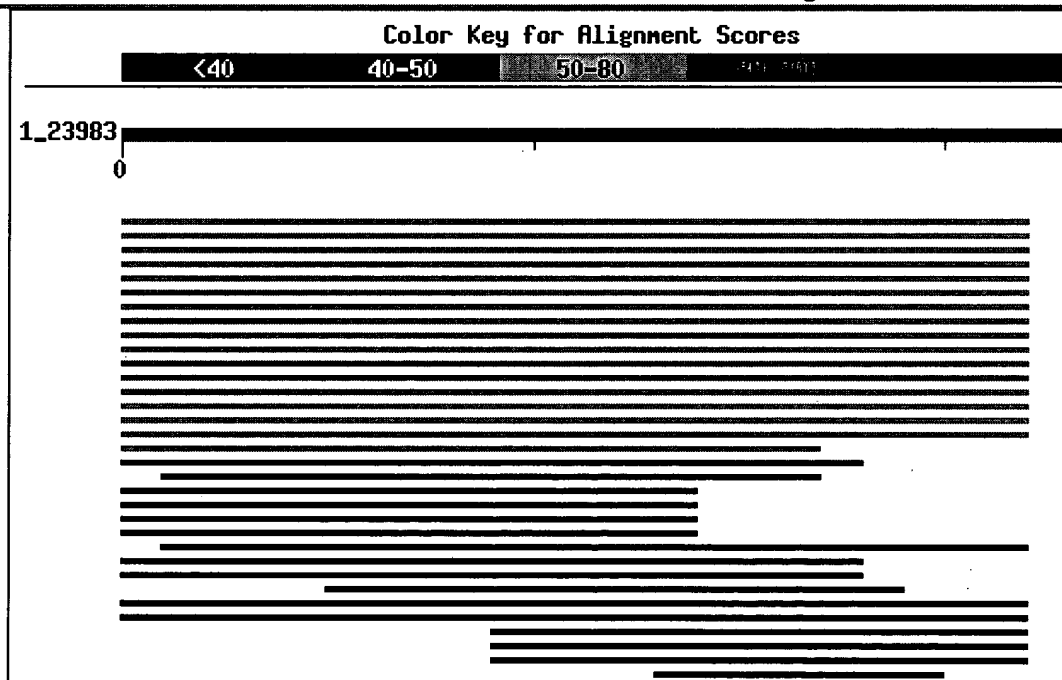
translations+PDB+SwissProt+PIR+PRF

1,438,044 sequences; 462,300,935 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 475 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments

**Related Structures**

Sequences producing significant alignments:

Score E
(bits) Value

gi 28883520 gb AAO49724.1	neuregulin 1 isoform 4 [Homo sap...	80	5e-15	
gi 284149 pir A43273	heregulin precursor, splice form alph...	80	5e-15	
gi 7513201 pir I38405	neu differentiation factor - human (...	80	5e-15	L
gi 7669526 ref NP_039258.1	neuregulin 1 isoform HRG-alpha;...	80	5e-15	L
gi 7513200 pir I38403	neu differentiation factor - human (...	80	5e-15	
gi 7669520 ref NP_039254.1	neuregulin 1 isoform ndf43; her...	80	5e-15	L
gi 22004079 tpg DAA00048.1	TPA: neuregulin 1 isoform HRG-a...	80	5e-15	L
gi 1633217 pdb 1HAF	Heregulin-Alpha Epidermal Growth Fact...	80	5e-15	S
gi 640060 pdb 1HRE	Heregulin-Alpha (Epidermal Growth Fact...	80	5e-15	S
gi 22004076 tpg DAA00045.1	TPA: neuregulin 1 isoform ndf43...	80	5e-15	L
gi 408399 gb AAA19949.1	neu differentiation factor	75	9e-14	L
gi 408383 gb AAA19941.1	neu differentiation factor >gi 408...	75	9e-14	L
gi 7514023 pir I61719	neu differentiation factor - rat >gi...	75	9e-14	L
gi 11066040 gb AAG28428.1 AF194439_1	SMDF neuregulin alpha ...	75	9e-14	L
gi 11066042 gb AAG28429.1 AF194440_1	SMDF neuregulin alpha ...	75	9e-14	L
gi 2459765 gb AAB71812.1	neuregulin [Mesocricetus auratus]	75	9e-14	
gi 2135345 pir S62676	heregulin isoform alpha 2 - human (f...	57	2e-08	
gi 9297012 sp O93383 NRG1_XENLA	Pro-neuregulin-1 precursor ...	43	3e-04	
gi 8132060 gb AAF73197.1 AF152001_1	Notch3 [Danio rerio]	33	0.38	L
gi 21361989 ref NP_078776.2	likely ortholog of mouse polyd...	33	0.51	L
gi 12738842 ref NP_073725.1	polydomain protein; D430029009...	33	0.51	L
gi 85085 pir A24420	notch protein - fruit fly (Drosophila ...	32	0.91	L
gi 24639454 ref NP_476859.2	Notch CG3936-PA [Drosophila me...	32	0.91	L
gi 157988 gb AAB59220.1	Notch growth factor [Drosophila me...	32	0.91	L
gi 18875406 ref NP_573502.1	crumbs homolog 1 [Mus musculus...	32	0.91	L
gi 4467343 emb CAB37610.1	EG:140G11.1 [Drosophila melanoga...	32	0.91	L
gi 18175295 gb AAL10682.1	CRB1 isoform II precursor [Homo ...	32	0.91	L
gi 6912322 ref NP_036208.1	crumbs homolog 1 [Homo sapiens]...	32	0.91	L
gi 13898380 gb AAK48712.1 AF307972_1	E-selectin [Equus caba...	31	2.2	
gi 7459690 pir T09059	notch4 - mouse >gi 2564947 gb AAB820...	31	2.2	
gi 6754874 ref NP_035059.1	Notch gene homolog 4; Notch gen...	31	2.2	L
gi 18252658 gb AAL66380.1 AF461685_1	Jedi-736 protein [Mus ...	31	2.2	L
gi 27503754 gb AAH42490.1	3110045G13Rik protein [Mus muscu...	31	2.2	L
gi 22779881 ref NP_082736.1	Jedi [Mus musculus] >gi 170172...	31	2.2	L
gi 17386053 gb AAL38571.1 AF444274_1	Jedi protein [Mus musc...	31	2.2	L
gi 1401160 gb AAC52630.1	Notch4	31	2.2	L
gi 28498994 ref XP_192820.2	similar to Notch gene homolog ...	30	4.0	L
gi 6679096 ref NP_032742.1	Notch gene homolog 3; Notch gen...	30	4.0	L
gi 27712336 ref XP_222675.1	similar to crumbs homolog 1 [M...	29	5.3	L
gi 7670249 dbj BAA95001.1	secretory protein containing EGF...	29	5.3	
gi 18858545 ref NP_571019.1	deltaC [Danio rerio] >gi 67395...	29	5.3	L
gi 12231943 gb AAG49316.1 AF315554_1	notch-like transmembra...	29	7.1	
gi 12231945 gb AAG49317.1 AF315555_1	notch-like transmembra...	29	7.1	
gi 24041035 ref NP_077719.2	notch 2 preproprotein [Homo sa...	29	9.6	L
gi 296611 emb CAA50556.1	receptor tyrosine kinase [Mus mus...	29	9.6	L
gi 17136480 ref NP_476727.1	slit CG8355-PC [Drosophila mel...	29	9.6	L
gi 11527997 gb AAG37073.1 AF315356_1	NOTCH2 protein [Homo s...	29	9.6	L
gi 17136484 ref NP_476729.1	slit CG8355-PB [Drosophila mel...	29	9.6	L
gi 103392 pir B36665	slit protein 2 precursor - fruit fly ...	29	9.6	
gi 6755785 ref NP_035717.1	tyrosine kinase receptor 1; D43...	29	9.6	L

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|28883520|gb|AAO49724.1| neuregulin 1 isoform 4 [Homo sapiens]
Length = 58

Score = 79.5 bits (180), Expect = 5e-15
Identities = 23/23 (100%), Positives = 23/23 (100%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
KCQPGFTGARCTENVPMKVQNQE
Sbjct: 22 KCQPGFTGARCTENVPMKVQNQE 44

☐ >gi|284149|pir||A43273 heregulin precursor, splice form alpha - human
Length = 640

Score = 79.5 bits (180), Expect = 5e-15
Identities = 23/23 (100%), Positives = 23/23 (100%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
KCQPGFTGARCTENVPMKVQNQE
Sbjct: 211 KCQPGFTGARCTENVPMKVQNQE 233

☐ >gi|7513201|pir||I38405 neu differentiation factor - human (fragment)
gi|408405|gb|AAA19952.1| neu differentiation factor
Length = 125

Score = 79.5 bits (180), Expect = 5e-15
Identities = 23/23 (100%), Positives = 23/23 (100%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
KCQPGFTGARCTENVPMKVQNQE
Sbjct: 89 KCQPGFTGARCTENVPMKVQNQE 111

☐ >gi|7669526|ref|NP_039258.1| neuregulin 1 isoform HRG-alpha; heregulin, alpha (p185-activator); glial growth factor; neu differentiation factor; sensory and motor neuron derived factor [Homo sapiens]
gi|9297018|sp|Q02297|NRG1 HUMAN Pro-neuregulin-1 precursor (Pro-NRG1) [Contains: Neu differentiation factor) (Heregulin) (HRG) (Breast cancer cell differentiation factor p45) (Acetylcholine receptor inducing activity) (ARIA) (Sensory and motor neuron-derived factor) (Glial growth factor)]
gi|183993|gb|AAA58638.1| heregulin-alpha
Length = 640

Score = 79.5 bits (180), Expect = 5e-15
Identities = 23/23 (100%), Positives = 23/23 (100%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
KCQPGFTGARCTENVPMKVQNQE
Sbjct: 211 KCQPGFTGARCTENVPMKVQNQE 233

☐ >gi|7513200|pir||I38403 neu differentiation factor - human (fragment)
gi|408401|gb|AAA19950.1| neu differentiation factor
Length = 350

Score = 79.5 bits (180), Expect = 5e-15
Identities = 23/23 (100%), Positives = 23/23 (100%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23

KCQPGFTGARCTENVPMKVQNQE

Sbjct: 18 KCQPGFTGARCTENVPMKVQNQE 40

gi|7669520|ref|NP_039254.1| neuregulin 1 isoform ndf43; heregulin, alpha (45kD, p185-activator); glial growth factor; neu differentiation factor; sensory and motor neuron derived factor [Homo sapiens]
gi|7513199|pir||I38404 neu differentiation factor - human
gi|408403|gb|AAA19951.1| neu differentiation factor
 Length = 462

Score = 79.5 bits (180), Expect = 5e-15
 Identities = 23/23 (100%), Positives = 23/23 (100%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
 KCQPGFTGARCTENVPMKVQNQE
 Sbjct: 211 KCQPGFTGARCTENVPMKVQNQE 233

gi|22004079|tpg|DAA00048.1| TPA: neuregulin 1 isoform HRG-alpha [Homo sapiens]
 Length = 640

Score = 79.5 bits (180), Expect = 5e-15
 Identities = 23/23 (100%), Positives = 23/23 (100%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
 KCQPGFTGARCTENVPMKVQNQE
 Sbjct: 211 KCQPGFTGARCTENVPMKVQNQE 233

gi|1633217|pdb|1HAF| **S** Heregulin-Alpha Epidermal Growth Factor-Like Domain, Nmr, Minimized Average Structure
gi|1633218|pdb|1HAE| **S** Heregulin-Alpha Epidermal Growth Factor-Like Domain, Nmr, 2 Structures
 Length = 63

Score = 79.5 bits (180), Expect = 5e-15
 Identities = 23/23 (100%), Positives = 23/23 (100%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
 KCQPGFTGARCTENVPMKVQNQE
 Sbjct: 35 KCQPGFTGARCTENVPMKVQNQE 57

gi|640060|pdb|1HRE| **S** Heregulin-Alpha (Epidermal Growth Factor-Like Domain) (Nmr, Minimized Average Structure)
gi|640061|pdb|1HRF| **S** Heregulin-Alpha (Epidermal Growth Factor-Like Domain) (Nmr, Structures)
 Length = 67

Score = 79.5 bits (180), Expect = 5e-15
 Identities = 23/23 (100%), Positives = 23/23 (100%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
 KCQPGFTGARCTENVPMKVQNQE
 Sbjct: 37 KCQPGFTGARCTENVPMKVQNQE 59

gi|22004076|tpg|DAA00045.1| TPA: neuregulin 1 isoform ndf43 [Homo sapiens]
 Length = 462

Score = 79.5 bits (180), Expect = 5e-15
 Identities = 23/23 (100%), Positives = 23/23 (100%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
 KCQPGFTGARCTENVPMKVQNQE

Sbjct: 211 KCQPGFTGARCTENVPMKVQNQE 233

>gi|408399|gb|AAA19949.1| neu differentiation factor
Length = 422

Score = 75.3 bits (170), Expect = 9e-14
Identities = 22/23 (95%), Positives = 22/23 (95%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
KCQPGFTGARCTENVPMKVQ QE

Sbjct: 211 KCQPGFTGARCTENVPMKVQTQE 233

>gi|408383|gb|AAA19941.1| neu differentiation factor
gi|408385|gb|AAA19942.1| neu differentiation factor
Length = 461

Score = 75.3 bits (170), Expect = 9e-14
Identities = 22/23 (95%), Positives = 22/23 (95%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
KCQPGFTGARCTENVPMKVQ QE

Sbjct: 211 KCQPGFTGARCTENVPMKVQTQE 233

>gi|7514023|pir||I61719 neu differentiation factor - rat
gi|408389|gb|AAA19944.1| neu differentiation factor
gi|408397|gb|AAA19948.1| neu differentiation factor
Length = 639

Score = 75.3 bits (170), Expect = 9e-14
Identities = 22/23 (95%), Positives = 22/23 (95%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
KCQPGFTGARCTENVPMKVQ QE

Sbjct: 211 KCQPGFTGARCTENVPMKVQTQE 233

>gi|11066040|gb|AAG28428.1|AF194439.1 SMDF neuregulin alpha 2a [Rattus norvegicus]
Length = 695

Score = 75.3 bits (170), Expect = 9e-14
Identities = 22/23 (95%), Positives = 22/23 (95%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
KCQPGFTGARCTENVPMKVQ QE

Sbjct: 267 KCQPGFTGARCTENVPMKVQTQE 289

>gi|11066042|gb|AAG28429.1|AF194440.1 SMDF neuregulin alpha 2b [Rattus norvegicus]
Length = 298

Score = 75.3 bits (170), Expect = 9e-14
Identities = 22/23 (95%), Positives = 22/23 (95%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
KCQPGFTGARCTENVPMKVQ QE

Sbjct: 81 KCQPGFTGARCTENVPMKVQTQE 103

>gi|2459765|gb|AAB71812.1| neuregulin [Mesocricetus auratus]
Length = 461

Score = 75.3 bits (170), Expect = 9e-14
Identities = 22/23 (95%), Positives = 22/23 (95%)

Query: 1 KCQPGFTGARCTENVPMKVQNQE 23
 KCQPGFTGARCTENVPMKVQ QE
 Sbjct: 211 KCQPGFTGARCTENVPMKVQTQE 233

>gi|2135345|pir||S62676 heregulin isoform alpha 2 - human (fragments)
 Length = 125

Score = 57.5 bits (128), Expect = 2e-08
 Identities = 17/18 (94%), Positives = 17/18 (94%)

Query: 1 KCQPGFTGARCTENVPMK 18
 KCQP FTGARCTENVPMK
 Sbjct: 108 KCQPQFTGARCTENVPMK 125

>gi|9297012|sp|O93383|NRG1_XENLA Pro-neuregulin-1 precursor (Pro-NRG1) [Contains:
 gi|3328217|gb|AAC26804.1| neuregulin alpha-1 [Xenopus laevis]
 Length = 677

Score = 43.5 bits (95), Expect = 3e-04
 Identities = 14/19 (73%), Positives = 17/19 (89%)

Query: 1 KCQPGFTGARCTENVPMKV 19
 KC+PGFTGARCTE P++V
 Sbjct: 221 KCKPGFTGARCTETDPLRV 239

>gi|8132060|gb|AAF73197.1|AF152001.1 Notch3 [Danio rerio]
 Length = 2468

Score = 33.3 bits (71), Expect = 0.38
 Identities = 13/21 (61%), Positives = 14/21 (66%), Gaps = 6/21 (28%)

Query: 2 CQPGFTGARC-TE-----NVP 16
 C PGFTGARC TE +VP
 Sbjct: 888 CLPGFTGARCATELNECQSV 908

Score = 28.2 bits (59), Expect = 13
 Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
 C PGFTG RC
 Sbjct: 1210 CPPGFTGERC 1219

Score = 28.2 bits (59), Expect = 13
 Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
 CQPGFTG C
 Sbjct: 471 CQPGFTGTMC 480

Score = 26.9 bits (56), Expect = 31
 Identities = 9/13 (69%), Positives = 11/13 (84%), Gaps = 1/13 (7%)

Query: 2 CQPGFTGARCTEN 14
 C+PG+TG RC EN
 Sbjct: 546 CEPGYTGYRC-EN 557

Score = 24.4 bits (50), Expect = 181
 Identities = 10/15 (66%), Positives = 11/15 (73%)

Query: 2 CQPGFTGARCTENVP 16

C+PGFTG C NVP
Sbjct: 926 CKPGFTGLLCETNVP 940

Score = 24.0 bits (49), Expect = 243
Identities = 7/10 (70%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C+PGFTG +C
Sbjct: 621 CKPGFTGTPQC 630

Score = 21.4 bits (43), Expect = 1415
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 2 CQPGFTG 8
C+PGFTG
Sbjct: 1250 CKPGFTG 1256

Score = 20.2 bits (40), Expect = 3419
Identities = 7/12 (58%), Positives = 8/12 (66%), Gaps = 2/12 (16%)

Query: 2 CQ--PGFTGARC 11
CQ G+TG RC
Sbjct: 393 CQCGRGYTGP RC 404

Score = 19.3 bits (38), Expect = 6156
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C G+TG RC
Sbjct: 1002 CPKGYTGPRC 1011

Score = 19.3 bits (38), Expect = 6156
Identities = 9/28 (32%), Positives = 9/28 (32%), Gaps = 17/28 (60%)

Query: 2 CQPGF-----TGARCT 12
CQ GF GARCT
Sbjct: 85 CQRGFRGQDCSLVDACATSPCANGARCT 112

Score = 18.9 bits (37), Expect = 8260
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 8 GARCT 12
GARCT
Sbjct: 1323 GARCT 1327

Score = 18.5 bits (36), Expect = 11083
Identities = 8/14 (57%), Positives = 9/14 (64%)

Query: 2 CQPGFTGARCTENV 15
C PGF G C +NV
Sbjct: 200 CLPGFRGHNCEDNV 213

>gi|21361989|ref|NP_078776.2| likely ortholog of mouse polydom [Homo sapiens]
gi|14042859|dbj|BAB55420.1| unnamed protein product [Homo sapiens]
Length = 1316

Score = 32.9 bits (70), Expect = 0.51
Identities = 11/14 (78%), Positives = 12/14 (85%), Gaps = 1/14 (7%)

Query: 1 KCQPGFTGARC-TE 13
 KCQPGF+G RC TE
 Sbjct: 1175 KCQPGFSGKRCETE 1188

Score = 27.8 bits (58), Expect = 17
 Identities = 10/15 (66%), Positives = 11/15 (73%)

Query: 1 KCQPGFTGARCTENV 15
 KC PGF G RC +NV
 Sbjct: 1099 KCPPGFLGTRCGKNV 1113

Score = 25.2 bits (52), Expect = 100
 Identities = 8/14 (57%), Positives = 10/14 (71%)


Query: 2 CQPGFTGARCTENV 15
 C G+TG RC EN+
 Sbjct: 1024 CPSGYTGQRCEENI 1037

Score = 20.2 bits (40), Expect = 3419
 Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
 C GFTG+ C
 Sbjct: 1138 CAAGFTGSHC 1147

Score = 17.6 bits (34), Expect = 19953
 Identities = 4/5 (80%), Positives = 4/5 (80%)

Query: 2 CQPGF 6
 C PGF
 Sbjct: 173 CHPGF 177

 >gi|12738842|ref|NP_073725.1| polydomain protein; D430029009Rik [Mus musculus]
 gi|11177164|gb|AAG32160.1|AF206329.1 polydom protein [Mus musculus]
 Length = 3567

Score = 32.9 bits (70), Expect = 0.51
 Identities = 11/14 (78%), Positives = 12/14 (85%), Gaps = 1/14 (7%)

Query: 1 KCQPGFTGARC-TE 13
 KCQPGF+G RC TE
 Sbjct: 1407 KCQPGFSGHRCETE 1420

Score = 27.8 bits (58), Expect = 17
 Identities = 10/15 (66%), Positives = 11/15 (73%)

Query: 1 KCQPGFTGARCTENV 15
 KC PGF G RC +NV
 Sbjct: 1331 KCPPGFLGTRCEKNV 1345

Score = 20.6 bits (41), Expect = 2548
 Identities = 8/12 (66%), Positives = 8/12 (66%), Gaps = 2/12 (16%)

Query: 2 CQ-P-GFTGARC 11
 CQ P GFTG C
 Sbjct: 1368 CQCPAGFTGTHC 1379

Score = 20.2 bits (40), Expect = 3419
Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PG+TG +C
Sbjct: 1218 CPPGYTGLKC 1227

Score = 18.5 bits (36), Expect = 11083
Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C G+TG+RC
Sbjct: 3518 CPTGWTGSRC 3527

gi|85085|pir|A24420 notch protein - fruit fly (*Drosophila melanogaster*)
gi|157993|gb|AAA28725.1| developmental protein
Length = 2703

Score = 32.0 bits (68), Expect = 0.91
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
CQPGF GARC
Sbjct: 1285 CQPGFVGARC 1294

Score = 28.2 bits (59), Expect = 13
Identities = 11/17 (64%), Positives = 12/17 (70%), Gaps = 2/17 (11%)

Query: 1 KCQ--PGFTGARCTENV 15
KCQ PGFTG C +NV
Sbjct: 700 KCQCVPGFTGQHCEKNV 716

Score = 25.2 bits (52), Expect = 100
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 5 GFTGARC 11
GFTGARC
Sbjct: 555 GFTGARC 561

Score = 24.0 bits (49), Expect = 243
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PGFTG +C
Sbjct: 514 CMPGFTGTQC 523

Score = 23.1 bits (47), Expect = 437
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PG+TG RC
Sbjct: 779 CPPGYTGKRC 788

Score = 22.7 bits (46), Expect = 586
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C GFTG RC
Sbjct: 476 CSQGFTGPRC 485

Score = 22.3 bits (45), Expect = 786
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C GFTG +C+E V
Sbjct: 1086 CPSGFTGKQCSEYV 1099

Score = 21.8 bits (44), Expect = 1055
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PGFTG C
Sbjct: 205 CPPGFTGDTTC 214

Score = 21.0 bits (42), Expect = 1899
Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 2/12 (16%)

Query: 2 CQ--PGFTGARC 11
CQ PG+TG +C
Sbjct: 815 CQCMPGYTQKC 826

Score = 21.0 bits (42), Expect = 1899
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PG+TG C
Sbjct: 590 CPPGYTGTSC 599

Score = 19.3 bits (38), Expect = 6156
Identities = 7/11 (63%), Positives = 9/11 (81%), Gaps = 1/11 (9%)

Query: 5 GFTGARC-TEN 14
G+TG RC T+N
Sbjct: 169 GYTGERCETKN 179

Score = 18.9 bits (37), Expect = 8260
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 2 CQPGFTG 8
C PG+TG
Sbjct: 627 CDPGYTG 633

gi|24639454|ref|NP_476859.2| Notch CG3936-PA [Drosophila melanogaster]
gi|17380387|sp|P07207|NOTC DROME Neurogenic locus Notch protein precursor
gi|10728440|gb|AAF45848.2| CG3936-PA [Drosophila melanogaster]
Length = 2703

Score = 32.0 bits (68), Expect = 0.91
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
CQPGF GARC
Sbjct: 1285 CQPGFVGARC 1294

Score = 28.2 bits (59), Expect = 13
Identities = 11/17 (64%), Positives = 12/17 (70%), Gaps = 2/17 (11%)

Query: 1 KCQ--PGFTGARCTENV 15
KCQ PGFTG C +NV
Sbjct: 700 KCQCVPGFTGQHCEKNV 716

Score = 25.2 bits (52), Expect = 100
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 5 GFTGARC 11
GFTGARC
Sbjct: 555 GFTGARC 561

Score = 24.0 bits (49), Expect = 243
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PGFTG +C
Sbjct: 514 CMPGFTGTQC 523

Score = 23.1 bits (47), Expect = 437
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PG+TG RC
Sbjct: 779 CPPGYTGKRC 788

Score = 22.7 bits (46), Expect = 586
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C GFTG RC
Sbjct: 476 CSQGFTGPRC 485

Score = 22.3 bits (45), Expect = 786
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C GFTG +C+E V
Sbjct: 1086 CPSGFTGKQCSEYV 1099

Score = 21.8 bits (44), Expect = 1055
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PGFTG C
Sbjct: 205 CPPGFTGDTC 214

Score = 21.0 bits (42), Expect = 1899
Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 2/12 (16%)

Query: 2 CQ--PGFTGARC 11
CQ PG+TG +C
Sbjct: 815 CQCMPGYTQKC 826

Score = 21.0 bits (42), Expect = 1899
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11


C PG+TG C
Sbjct: 590 CPPGYTGTSC 599

Score = 19.3 bits (38), Expect = 6156
Identities = 7/11 (63%), Positives = 9/11 (81%), Gaps = 1/11 (9%)

Query: 5 GFTGARC-TEN 14
G+TG RC T+N
Sbjct: 169 GYTGERCETKN 179

Score = 18.9 bits (37), Expect = 8260
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 2 CQPGFTG 8
C PG+TG
Sbjct: 627 CDPGYTG 633

 >gi|157988|gb|AAB59220.1| Notch growth factor [Drosophila melanogaster]
Length = 2703

Score = 32.0 bits (68), Expect = 0.91
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
CQPGF GARC
Sbjct: 1285 CQPGFVGARC 1294

Score = 28.2 bits (59), Expect = 13
Identities = 11/17 (64%), Positives = 12/17 (70%), Gaps = 2/17 (11%)

Query: 1 KCQ--PGFTGARCTENV 15
KCQ PGFTG C +NV
Sbjct: 700 KCQCVPGFTGQHCEKNV 716

Score = 25.2 bits (52), Expect = 100
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 5 GFTGARC 11
GFTGARC
Sbjct: 555 GFTGARC 561

Score = 24.0 bits (49), Expect = 243
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PGFTG +C
Sbjct: 514 CMPGFTGTQC 523

Score = 23.1 bits (47), Expect = 437
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PG+TG RC
Sbjct: 779 CPPGYTGKRC 788

Score = 22.7 bits (46), Expect = 586
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C GFTG RC
Sbjct: 476 CSQGFTGPRC 485

Score = 22.3 bits (45), Expect = 786
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C GFTG +C+E V
Sbjct: 1086 CPSGFTGKQCSEYV 1099

Score = 21.8 bits (44), Expect = 1055
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PGFTG C
Sbjct: 205 CPPGFTGDTTC 214

Score = 21.0 bits (42), Expect = 1899
Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 2/12 (16%)

Query: 2 CQ--PGFTGARC 11
CQ PG+TG +C
Sbjct: 815 CQCMPGYTGQKC 826

Score = 21.0 bits (42), Expect = 1899
Identities = 6/10 (60%), Positives = 7/10 (70%)


Query: 2 CQPGFTGARC 11
C PG+TG C
Sbjct: 590 CPPGYTGTSC 599

Score = 19.3 bits (38), Expect = 6156
Identities = 7/11 (63%), Positives = 9/11 (81%), Gaps = 1/11 (9%)

Query: 5 GFTGARC-TEN 14
G+TG RC T+N
Sbjct: 169 GYTGERCETKN 179

Score = 18.9 bits (37), Expect = 8260
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 2 CQPGFTG 8
C PG+TG
Sbjct: 627 CDPGYTG 633

 >gi|18875406|ref|NP_573502.1| crumbs homolog 1 [Mus musculus]
gi|18182323|gb|AAL65131.1|AF406641 1 crumbs-like protein 1 precursor [Mus musculus]
Length = 1405

Score = 32.0 bits (68), Expect = 0.91
Identities = 10/14 (71%), Positives = 11/14 (78%)

Query: 2 CQPGFTGARCTENV 15
CQPGFTG C E+V
Sbjct: 384 CQPGFTGIHCEEDV 397

Score = 23.5 bits (48), Expect = 325

Identities = 7/12 (58%), Positives = 9/12 (75%)


Query: 4 PGFTGARCTENV 15
PGFTG C E++
Sbjct: 1286 PGFTGEWCEEDI 1297

Score = 22.3 bits (45), Expect = 786
Identities = 7/10 (70%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C+PG+TGA C
Sbjct: 326 CRPGYTGALC 335

Score = 21.0 bits (42), Expect = 1899
Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C+PG+TG C
Sbjct: 1201 CEPGYTGVNC 1210

 >gi|4467343|emb|CAB37610.1| EG:140G11.1 [Drosophila melanogaster]
Length = 2704

Score = 32.0 bits (68), Expect = 0.91
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
CQPGF GARC
Sbjct: 1285 CQPGFVGARC 1294

Score = 28.2 bits (59), Expect = 13
Identities = 11/17 (64%), Positives = 12/17 (70%), Gaps = 2/17 (11%)

Query: 1 KCQ--PGFTGARCTENV 15
KCQ PGFTG C +NV
Sbjct: 700 KCQCVPGFTGQHCEKNV 716

Score = 25.2 bits (52), Expect = 100
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 5 GFTGARC 11
GFTGARC
Sbjct: 555 GFTGARC 561

Score = 24.0 bits (49), Expect = 243
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PGFTG +C
Sbjct: 514 CMPGFTGTQC 523

Score = 23.1 bits (47), Expect = 437
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PG+TG RC
Sbjct: 779 CPPGYTGKRC 788

Score = 22.7 bits (46), Expect = 586
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C GFTG RC
Sbjct: 476 CSQGFTGPRC 485

Score = 22.3 bits (45), Expect = 786
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C GFTG +C+E V
Sbjct: 1086 CPSGFTGKCSEYV 1099

Score = 21.8 bits (44), Expect = 1055
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PGFTG C
Sbjct: 205 CPPGFTGDTC 214

Score = 21.0 bits (42), Expect = 1899
Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 2/12 (16%)

Query: 2 CQ--PGFTGARC 11
CQ PG+TG +C
Sbjct: 815 CQCMPGYTGQKC 826

Score = 21.0 bits (42), Expect = 1899
Identities = 6/10 (60%), Positives = 7/10 (70%)


Query: 2 CQPGFTGARC 11
C PG+TG C
Sbjct: 590 CPPGYTGTSC 599

Score = 19.3 bits (38), Expect = 6156
Identities = 7/11 (63%), Positives = 9/11 (81%), Gaps = 1/11 (9%)

Query: 5 GFTGARC-TEN 14
G+TG RC T+N
Sbjct: 169 GYTGERCETKN 179

Score = 18.9 bits (37), Expect = 8260
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 2 CQPGFTG 8
C PG+TG
Sbjct: 627 CDPGYTG 633

 >gi|18175295|gb|AAL10682.1| CRB1 isoform II precursor [Homo sapiens]
Length = 1406

Score = 32.0 bits (68), Expect = 0.91
Identities = 10/14 (71%), Positives = 11/14 (78%)

Query: 2 CQPGFTGARCTENV 15
CQPGFTG C E+V
Sbjct: 385 CQPGFTGIHCEEDV 398

Score = 24.4 bits (50), Expect = 181
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C+PGFTG C
Sbjct: 1285 CRPGFTGEWC 1294

Score = 21.4 bits (43), Expect = 1415
Identities = 6/8 (75%), Positives = 8/8 (100%)

Query: 4 PGFTGARC 11
PG+TGA+C
Sbjct: 329 PGYTGAQC 336

Score = 21.0 bits (42), Expect = 1899
Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C+PG+TG C
Sbjct: 1202 CEPGYTGVNC 1211

Score = 20.2 bits (40), Expect = 3419
Identities = 6/11 (54%), Positives = 8/11 (72%)

Query: 1 KCQPGFTGARC 11
KC PG++G C
Sbjct: 97 KCPPGYSGTIC 107

Score = 18.0 bits (35), Expect = 14871
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 5 GFTGARC 11
GFTG C
Sbjct: 292 GFTGTHC 298

gi|6912322|ref|NP_036208.1| crumbs homolog 1 [Homo sapiens]
gi|17374421|sp|P82279|CRBH HUMAN Crumbs protein homolog 1 precursor
gi|6014482|gb|AAF01361.1|AF154671.1 CRB1 [Homo sapiens]
gi|18175289|gb|AAL10681.1| CRB1 isoform I precursor [Homo sapiens]
Length = 1376

Score = 32.0 bits (68), Expect = 0.91
Identities = 10/14 (71%), Positives = 11/14 (78%)

Query: 2 CQPGFTGARCTENV 15
CQPGFTG C E+V
Sbjct: 385 CQPGFTGIHCEEDV 398

Score = 24.4 bits (50), Expect = 181
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C+PGFTG C
Sbjct: 1285 CRPGFTGEWC 1294

Score = 21.4 bits (43), Expect = 1415
Identities = 6/8 (75%), Positives = 8/8 (100%)

Query: 4 PGFTGARC 11
PG+TGA+C
Sbjct: 329 PGYTGAQC 336

Score = 21.0 bits (42), Expect = 1899
Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C+PG+TG C
Sbjct: 1202 CEPGYTGVNC 1211

Score = 20.2 bits (40), Expect = 3419
Identities = 6/11 (54%), Positives = 8/11 (72%)

Query: 1 KCQPGFTGARC 11
KC PG++G C
Sbjct: 97 KCPPGYSGTIC 107

Score = 18.0 bits (35), Expect = 14871
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 5 GFTGARC 11
GFTG C
Sbjct: 292 GFTGTHC 298

☐ >gi|13898380|gb|AAK48712.1|AF307972.1 E-selectin [Equus caballus]
Length = 610

Score = 30.8 bits (65), Expect = 2.2
Identities = 14/24 (58%), Positives = 14/24 (58%), Gaps = 6/24 (25%)

Query: 2 CQPGFTGARCTENVPMKV--QNQE 23
C PGFTG RC E V V Q QE
Sbjct: 164 CHPGFTGLRC-EQV---VTCQAQE 183

Score = 17.6 bits (34), Expect = 19953
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 19 VQNQE 23
+QNQE
Sbjct: 50 IQNQE 54

☐ >gi|7459690|pir|T09059 notch4 - mouse
gi|2564947|gb|AAB82004.1| notch4 [Mus musculus]
Length = 1964

Score = 30.8 bits (65), Expect = 2.2
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C PGFTGARC
Sbjct: 536 CLPGFTGARC 545

Score = 25.2 bits (52), Expect = 100
Identities = 7/10 (70%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C PG+TG+RC
Sbjct: 460 CLPGYTGSRC 469

Score = 23.5 bits (48), Expect = 325
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C GFTG RC
Sbjct: 102 CPSGFTGDRC 111

Score = 22.7 bits (46), Expect = 586
Identities = 10/16 (62%), Positives = 12/16 (75%), Gaps = 2/16 (12%)

Query: 2 CQPGFTGARCTENVPM 17
C+PGFTG C E VP+
Sbjct: 612 CRPGFTGQLC-E-VPL 625

Score = 22.3 bits (45), Expect = 786
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PGF G RC
Sbjct: 990 CPPGFVGLRC 999

Score = 21.8 bits (44), Expect = 1055
Identities = 6/10 (60%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
CQPG++G+ C
Sbjct: 417 CQPGYSGSTC 426

Score = 21.4 bits (43), Expect = 1415
Identities = 11/18 (61%), Positives = 11/18 (61%), Gaps = 4/18 (22%)

Query: 2 CQ--PGFTGARCTENVPM 17
CQ PG TG RC E V M
Sbjct: 1028 CQCLPGHTGQRC-E-VEM 1043

Score = 21.4 bits (43), Expect = 1415
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 CQPGFTG 8
C PGFTG
Sbjct: 261 CPPGFTG 267

Score = 20.6 bits (41), Expect = 2548
Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PG+TG+ C
Sbjct: 829 CSPGYTGSSC 838

Score = 20.2 bits (40), Expect = 3419
Identities = 6/10 (60%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C+PG+TG +C
Sbjct: 142 CEPGWTGEQC 151

>gi|6754874|ref|NP_035059.1| Notch gene homolog 4; Notch gene homolog 4, (Droso
 musculus]
gi|2506381|sp|P31695|NTC4 MOUSE Neurogenic locus notch homolog protein 4 precursor
 [Contains: Transforming protein Int-3]
gi|1714084|gb|AAB38377.1| [Mus musculus activated Int-3 mammary gene mRNA, comple
 gene product
 Length = 1964

Score = 30.8 bits (65), Expect = 2.2
 Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
 C PGFTGARC
 Sbjct: 536 CLPGFTGARC 545

Score = 25.2 bits (52), Expect = 100
 Identities = 7/10 (70%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
 C PG+TG+RC
 Sbjct: 460 CLPGYTGSRC 469

Score = 23.5 bits (48), Expect = 325
 Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
 C GFTG RC
 Sbjct: 102 CPSGFTGDRC 111

Score = 22.7 bits (46), Expect = 586
 Identities = 10/16 (62%), Positives = 12/16 (75%), Gaps = 2/16 (12%)

Query: 2 CQPGFTGARCTENVPM 17
 C+PGFTG C E VP+
 Sbjct: 612 CRPGFTGQLC-E-VPL 625

Score = 22.3 bits (45), Expect = 786
 Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
 C PGF G RC
 Sbjct: 990 CPPGFVGLRC 999

Score = 21.8 bits (44), Expect = 1055
 Identities = 6/10 (60%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
 CQPG++G+ C
 Sbjct: 417 CQPGYSGSTC 426

Score = 21.4 bits (43), Expect = 1415
 Identities = 11/18 (61%), Positives = 11/18 (61%), Gaps = 4/18 (22%)

Query: 2 CQ--PGFTGARCTENVPM 17
 CQ PG TG RC E V M
 Sbjct: 1028 CQCLPGHTGQRC-E-VEM 1043

Score = 21.4 bits (43), Expect = 1415

Identities = 6/7 (85%), Positives = 6/7 (85%)


Query: 2 CQPGFTG 8
C PGFTG
Sbjct: 261 CPPGFTG 267

Score = 20.6 bits (41), Expect = 2548
Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PG+TG+ C
Sbjct: 829 CSPGYTGSSC 838

Score = 20.2 bits (40), Expect = 3419
Identities = 6/10 (60%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C+PG+TG +C
Sbjct: 142 CEPGWTGEQC 151

 >gi|18252658|gb|AAL66380.1|AF461685 1 Jedi-736 protein [Mus musculus]
Length = 747

Score = 30.8 bits (65), Expect = 2.2
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 2 CQPGFTGARCTE 13
C+ GFTG RCTE
Sbjct: 334 CEHGFTGDRCTE 345

Score = 21.8 bits (44), Expect = 1055
Identities = 7/12 (58%), Positives = 8/12 (66%)

Query: 2 CQPGFTGARCTE 13
C PG+ G RC E
Sbjct: 291 CAPGYIGDRCQE 302

Score = 21.4 bits (43), Expect = 1415
Identities = 8/15 (53%), Positives = 10/15 (66%)


Query: 2 CQPGFTGARCTENVP 16
CQPG+ G C E+ P
Sbjct: 380 CQPGWAGLHCNESP 394

Score = 20.6 bits (41), Expect = 2548
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PG+TG C
Sbjct: 423 CAPGYTGPHC 432

Score = 18.9 bits (37), Expect = 8260
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
CQ G+ G RC
Sbjct: 552 CQAGWMGTRC 561

 >gi|27503754|gb|AAH42490.1| 3110045G13Rik protein [Mus musculus]
Length = 1004

Score = 30.8 bits (65), Expect = 2.2
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 2 CQPGFTGARCTE 13
C+ GFTG RCTE
Sbjct: 334 CEHGFTGDRCTE 345

Score = 21.8 bits (44), Expect = 1055
Identities = 7/12 (58%), Positives = 8/12 (66%)


Query: 2 CQPGFTGARCTE 13
C PG+ G RC E
Sbjct: 291 CAPGYIGDRCQE 302

Score = 20.6 bits (41), Expect = 2548
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PG+TG C
Sbjct: 393 CAPGYTGPHC 402

Score = 18.9 bits (37), Expect = 8260
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
CQ G+ G RC
Sbjct: 522 CQAGWMGTRC 531

 >gi|22779881|ref|NP_082736.1| Jedi [Mus musculus]
gi|17017251|gb|AAL33583.1|AF440279_1 MEGF12 [Mus musculus]
gi|26343539|dbj|BAC35426.1| unnamed protein product [Mus musculus]
Length = 1034

Score = 30.8 bits (65), Expect = 2.2
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 2 CQPGFTGARCTE 13
C+ GFTG RCTE
Sbjct: 334 CEHGFTGDRCTE 345

Score = 21.8 bits (44), Expect = 1055
Identities = 7/12 (58%), Positives = 8/12 (66%)

Query: 2 CQPGFTGARCTE 13
C PG+ G RC E
Sbjct: 291 CAPGYIGDRCQE 302

Score = 21.4 bits (43), Expect = 1415
Identities = 8/15 (53%), Positives = 10/15 (66%)

Query: 2 CQPGFTGARCTENVP 16
CQPG+ G C E+ P
Sbjct: 380 CQPGWAGLHCNЕСP 394


Score = 20.6 bits (41), Expect = 2548

Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PG+TG C
Sbjct: 423 CAPGYTGPHC 432

Score = 18.9 bits (37), Expect = 8260
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
CQ G+ G RC
Sbjct: 552 CQAGWMGTRC 561

 >gi|17386053|gb|AAL38571.1|AF444274.1 Jedi protein [Mus musculus]
Length = 1034

Score = 30.8 bits (65), Expect = 2.2
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 2 CQPGFTGARCTE 13
C+ GFTG RCTE
Sbjct: 334 CEHGFTGDRCTE 345

Score = 21.8 bits (44), Expect = 1055
Identities = 7/12 (58%), Positives = 8/12 (66%)

Query: 2 CQPGFTGARCTE 13
C PG+ G RC E
Sbjct: 291 CAPGYIGDRCQE 302

Score = 21.4 bits (43), Expect = 1415
Identities = 8/15 (53%), Positives = 10/15 (66%)


Query: 2 CQPGFTGARCTENVP 16
CQPG+ G C E+ P
Sbjct: 380 CQPGWAGLHCNЕСP 394

Score = 20.6 bits (41), Expect = 2548
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PG+TG C
Sbjct: 423 CAPGYTGPHC 432

Score = 18.9 bits (37), Expect = 8260
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
CQ G+ G RC
Sbjct: 552 CQAGWMGTRC 561

 >gi|1401160|gb|AAC52630.1| Notch4
Length = 1964

Score = 30.8 bits (65), Expect = 2.2
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C PGFTGARC

Sbjct: 536 CLPGFTGARC 545

Score = 25.2 bits (52), Expect = 100
Identities = 7/10 (70%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C PG+TG+RC

Sbjct: 460 CLPGYTGSRC 469

Score = 23.5 bits (48), Expect = 325
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C GFTG RC

Sbjct: 102 CPSGFTGDRC 111

Score = 22.7 bits (46), Expect = 586
Identities = 10/16 (62%), Positives = 12/16 (75%), Gaps = 2/16 (12%)

Query: 2 CQPGFTGARCTENVPM 17
C+PGFTG C E VP+

Sbjct: 612 CRPGFTGQLC-E-VPL 625

Score = 22.3 bits (45), Expect = 786
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PGF G RC

Sbjct: 990 CPPGFFVGLRC 999

Score = 21.8 bits (44), Expect = 1055
Identities = 6/10 (60%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
CQPG++G+ C

Sbjct: 417 CQPGYSGSTC 426

Score = 21.4 bits (43), Expect = 1415
Identities = 11/18 (61%), Positives = 11/18 (61%), Gaps = 4/18 (22%)

Query: 2 CQ--PGFTGARCTENVPM 17
CQ PG TG RC E V M

Sbjct: 1028 CQCLPGHTGQRC-E-VEM 1043

Score = 21.4 bits (43), Expect = 1415
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 CQPGFTG 8
C PGFTG

Sbjct: 261 CPPGFTG 267

Score = 20.6 bits (41), Expect = 2548
Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PG+TG+ C

Sbjct: 829 CSPGYTGSSC 838

Score = 20.2 bits (40), Expect = 3419
Identities = 6/10 (60%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C+PG+TG +C
Sbjct: 142 CEPGWTGEQC 151

gi|28498994|ref|XP_192820.2| similar to Notch gene homolog 3, (Drosophila) [Mus
Length = 1319

Score = 29.9 bits (63), Expect = 4.0
Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PGFTG RC
Sbjct: 809 CHPGFTGPRC 818

Score = 27.8 bits (58), Expect = 17
Identities = 10/14 (71%), Positives = 10/14 (71%), Gaps = 2/14 (14%)

Query: 2 CQPGFTGARCTENV 15
CQPGFTG C NV
Sbjct: 220 CQPGFTGPLC--NV 231

Score = 21.8 bits (44), Expect = 1055
Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C+PG+TG C
Sbjct: 525 CRPGYTGTTC 534

Score = 21.8 bits (44), Expect = 1055
Identities = 6/12 (50%), Positives = 11/12 (91%)

Query: 2 CQPGFTGARCTE 13
C+PG++G RC++
Sbjct: 295 CEPGWGPRCSQ 306

Score = 19.7 bits (39), Expect = 4588
Identities = 6/10 (60%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C+ GFTG++C
Sbjct: 563 CREGFTGSQC 572

Score = 19.7 bits (39), Expect = 4588
Identities = 7/14 (50%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C PG+ G RC ++V
Sbjct: 373 CPPGWQGPCRCQDV 386

Score = 19.3 bits (38), Expect = 6156
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PG+TG C

Sbjct: 768 CPPGYTGLHC 777

Score = 18.5 bits (36), Expect = 11083
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 5 GFTGARC 11

GF G RC

Sbjct: 453 GFAGPRC 459

|>gi|6679096|ref|NP_032742.1|
musculus]

Notch gene homolog 3; Notch gene homolog 3, (Drosophila)

gi|2494294|sp|Q61982|NTC3 MOUSE

Neurogenic locus notch homolog protein 3 precursor

gi|631742|pir|S45306 notch 3 protein - mouse

gi|483581|emb|CAA52776.1|

Notch 3 [Mus musculus]

Length = 2318

Score = 29.9 bits (63), Expect = 4.0
Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11

C PGFTG RC

Sbjct: 1235 CHPGFTGPRC 1244

Score = 27.8 bits (58), Expect = 17
Identities = 10/14 (71%), Positives = 10/14 (71%), Gaps = 2/14 (14%)

Query: 2 CQPGFTGARCTENV 15

CQPGFTG C NV

Sbjct: 646 CQPGFTGPLC--NV 657

Score = 24.0 bits (49), Expect = 243
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15

C PGFTG C ++V

Sbjct: 380 CPPGFTGGACDQDV 393

Score = 23.5 bits (48), Expect = 325
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11

C PG+TG RC

Sbjct: 571 CAPGYTGIRC 580

Score = 21.8 bits (44), Expect = 1055
Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11

C+PG+TG C

Sbjct: 951 CRPGYTGTHC 960

Score = 21.8 bits (44), Expect = 1055
Identities = 6/12 (50%), Positives = 11/12 (91%)

Query: 2 CQPGFTGARCTE 13

C+PG++G RC++

Sbjct: 721 CEPGWSGPRCSQ 732

Score = 20.6 bits (41), Expect = 2548
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C P +TG CTE+V
Sbjct: 263 CPPEWTGQFCTEDV 276

Score = 20.2 bits (40), Expect = 3419
Identities = 7/12 (58%), Positives = 8/12 (66%), Gaps = 2/12 (16%)

Query: 2 CQ--PGFTGARC 11
CQ G+TG RC
Sbjct: 418 CQCGRGYTGPRC 429

Score = 19.7 bits (39), Expect = 4588
Identities = 6/10 (60%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C+ GFTG++C
Sbjct: 989 CREGFTGSQC 998

Score = 19.7 bits (39), Expect = 4588
Identities = 7/14 (50%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C PG+ G RC ++V
Sbjct: 799 CPPGWQGPRCQQDV 812

Score = 19.3 bits (38), Expect = 6156
Identities = 6/10 (60%), Positives = 7/10 (70%)


Query: 2 CQPGFTGARC 11
C PG+TG C
Sbjct: 1194 CPPGYTGLHC 1203

Score = 18.5 bits (36), Expect = 11083
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 5 GFTGARC 11
GF G RC
Sbjct: 879 GFAGPRC 885

Score = 17.6 bits (34), Expect = 19953
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PG+ G RC
Sbjct: 68 CLPGWVGERC 77

 >gi|27712336|ref|XP_222675.1| similar to crumbs homolog 1 [Mus musculus] [Rattus]
Length = 1104

Score = 29.5 bits (62), Expect = 5.3
Identities = 9/14 (64%), Positives = 11/14 (78%)


Query: 2 CQPGFTGARCTENV 15
C+PGFTG C EN+
Sbjct: 847 CRPGFTGEWCEENI 860

Score = 21.0 bits (42), Expect = 1899
Identities = 6/10 (60%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C+PG+TG C
Sbjct: 764 CEPGYTGGNC 773

Score = 19.7 bits (39), Expect = 4588
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C PG++GA C NV
Sbjct: 727 CLPGWSGAHCEINV 740

 >gi|7670249|dbj|BAA95001.1| secretory protein containing EGF domain [Xenopus laevis]
Length = 778

Score = 29.5 bits (62), Expect = 5.3
Identities = 9/14 (64%), Positives = 12/14 (85%)

Query: 2 CQPGFTGARCTENV 15
CQPGFTG+ C+ N+
Sbjct: 415 CQPGFTGSNCSVNI 428

Score = 26.9 bits (56), Expect = 31
Identities = 9/14 (64%), Positives = 9/14 (64%), Gaps = 4/14 (28%)


Query: 1 KCQPGFTGARCTEN 14
KCQPGF G EN
Sbjct: 538 KCQPGFAG----EN 547

Score = 23.1 bits (47), Expect = 437
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 2 CQPGFTG 8
C+PGFTG
Sbjct: 166 CEPGFTG 172


Score = 21.8 bits (44), Expect = 1055
Identities = 7/11 (63%), Positives = 7/11 (63%), Gaps = 3/11 (27%)

Query: 2 CQPGFTGARCT 12
CQPGF CT
Sbjct: 95 CQPGFN---CT 102

 >gi|18858545|ref|NP_571019.1| deltaC [Danio rerio]
gi|6739553|gb|AAF27299.1| DeltaC [Danio rerio]
Length = 664

Score = 29.5 bits (62), Expect = 5.3
Identities = 8/10 (80%), Positives = 10/10 (100%)

Query: 2 CQPGFTGARC 11
C+PGFTG+RC
Sbjct: 408 CRPGFTGSRC 417

 >gi|12231943|gb|AAG49316.1|AF315554.1 notch-like transmembrane receptor [Caenorhabditis elegans]
Length = 1270

Score = 29.1 bits (61), Expect = 7.1
Identities = 12/23 (52%), Positives = 14/23 (60%), Gaps = 4/23 (17%)


Query: 1 KCQPGFTGARC----TENVPMKV 19
KC P FTG RC T +PM+V
Sbjct: 347 KCPPSFTGDRCELNRTAVLPMEV 369

Score = 23.1 bits (47), Expect = 437
Identities = 7/11 (63%), Positives = 8/11 (72%)

Query: 5 GFTGARCTENV 15
G+TG RC E V
Sbjct: 470 GYTGTTCQEKV 480

Score = 22.7 bits (46), Expect = 586
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C+PGFTG C
Sbjct: 258 CKPGFTGTNC 267


 >gi|12231945|gb|AAG49317.1|AF315555.1 notch-like transmembrane receptor [Caenorhal
Length = 963

Score = 29.1 bits (61), Expect = 7.1
Identities = 12/23 (52%), Positives = 14/23 (60%), Gaps = 4/23 (17%)

Query: 1 KCQPGFTGARC----TENVPMKV 19
KC P FTG RC T +PM+V
Sbjct: 40 KCPPSFTGDRCELNRTAVLPMEV 62

Score = 23.1 bits (47), Expect = 437
Identities = 7/11 (63%), Positives = 8/11 (72%)

Query: 5 GFTGARCTENV 15
G+TG RC E V
Sbjct: 163 GYTGTTCQEKV 173

 >gi|24041035|ref|NP_077719.2| notch 2 preproprotein [Homo sapiens]
Length = 2471

Score = 28.6 bits (60), Expect = 9.6
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C PGF+GARC
Sbjct: 1333 CPPGFSGARC 1342

Score = 26.5 bits (55), Expect = 42
Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PGFTG RC
Sbjct: 670 CSPGFTGQRC 679

Score = 24.8 bits (51), Expect = 135
Identities = 9/14 (64%), Positives = 9/14 (64%), Gaps = 1/14 (7%)

Query: 1 KCQPGFTGARCTEN 14

KCQ GF G C EN

Sbjct: 974 KCQAGFDGVHC-EN 986

Score = 24.0 bits (49), Expect = 243
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PGF G RC
Sbjct: 1252 CLPGFAGERC 1261

Score = 23.5 bits (48), Expect = 325
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PGFTG +C
Sbjct: 937 CLPGFTGDKC 946

Score = 22.3 bits (45), Expect = 786
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C G+ GA CTE+V
Sbjct: 403 CPQGYKGADCTEDV 416

Score = 21.4 bits (43), Expect = 1415
Identities = 9/16 (56%), Positives = 10/16 (62%), Gaps = 2/16 (12%)

Query: 2 CQ--PGFTGARCTENV 15
CQ GFTG C EN+
Sbjct: 556 CQCATGFTGVLCENI 571

Score = 21.4 bits (43), Expect = 1415
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 CQPGFTG 8
C PGFTG
Sbjct: 520 CPPGFTG 526

Score = 21.0 bits (42), Expect = 1899
Identities = 7/11 (63%), Positives = 8/11

Query: 1 KCQPGFTGARC 11
KC GFTG +C
Sbjct: 169 KCLTGFTGQKC 179

Score = 20.2 bits (40), Expect = 3419
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 CQPGFTG 8
CQ GFTG
Sbjct: 133 CQVGFTG 139

Score = 19.3 bits (38), Expect = 6156
Identities = 7/11 (63%), Positives = 8/11 (72%)

Query: 2 CQPGFTGARCT 12
C PG+ G RCT

Sbjct: 861 CAPGWQQRCT 871

Score = 19.3 bits (38), Expect = 6156
Identities = 6/12 (50%), Positives = 9/12 (75%)

Query: 2 CQPGFTGARCTE 13
C PG+ GA C++

Sbjct: 595 CNPGYMGAIKSD 606

Score = 19.3 bits (38), Expect = 6156
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C P +TG CTE+V
Sbjct: 286 CPPQWTGQFCTEDV 299

>gi|296611|emb|CAA50556.1| receptor tyrosine kinase [Mus musculus]
Length = 1134

Score = 28.6 bits (60), Expect = 9.6
Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PGFTG RC
Sbjct: 244 CPPGFTGTRC 253

>gi|17136480|ref|NP_476727.1| slit CG8355-PC [Drosophila melanogaster]
gi|7303028|gb|AAF58097.1| CG8355-PC [Drosophila melanogaster]
Length = 1504

Score = 28.6 bits (60), Expect = 9.6
Identities = 9/12 (75%), Positives = 10/12 (83%), Gaps = 2/12 (16%)

Query: 2 CQ--PGFTGARC 11
CQ PG+TGARC
Sbjct: 995 CQCAPGYTGARC 1006

Score = 25.2 bits (52), Expect = 100
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
CQ GF G CT+N+
Sbjct: 1076 CQAGFHGTNCTDNI 1089

Score = 23.1 bits (47), Expect = 437
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 2 CQPGFTG 8
CQPGF+G
Sbjct: 1036 CQPGFSG 1042

Score = 20.6 bits (41), Expect = 2548
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PG+TG C
Sbjct: 1163 CHPGYTGWKC 1172

Score = 17.6 bits (34), Expect = 19953
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 CQPGF 6
CQPG+
Sbjct: 958 CQPGY 962

gi|11527997|gb|AAG37073.1|AF315356.1 NOTCH2 protein [Homo sapiens]
Length = 2471

Score = 28.6 bits (60), Expect = 9.6
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 2 CQPGFTGARC 11
C PGF+GARC
Sbjct: 1333 CPPGFSGARC 1342

Score = 26.5 bits (55), Expect = 42
Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PGFTG RC
Sbjct: 670 CSPGFTGQRC 679

Score = 24.8 bits (51), Expect = 135
Identities = 9/14 (64%), Positives = 9/14 (64%), Gaps = 1/14 (7%)

Query: 1 KCQPGFTGARCTEN 14
KCQ GF G C EN
Sbjct: 974 KCQAGFDGVHC-EN 986

Score = 24.0 bits (49), Expect = 243
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PGF G RC
Sbjct: 1252 CLPGFAGERC 1261

Score = 23.5 bits (48), Expect = 325
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PGFTG +C
Sbjct: 937 CLPGFTGDKC 946

Score = 22.3 bits (45), Expect = 786
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C G+ GA CTE+V
Sbjct: 403 CPQGYKGADCTEDV 416

Score = 21.4 bits (43), Expect = 1415
Identities = 9/16 (56%), Positives = 10/16 (62%), Gaps = 2/16 (12%)

Query: 2 CQ--PGFTGARCTENV 15
CQ GFTG C EN+
Sbjct: 556 CQCATGFTGVLCEENI 571

Score = 21.4 bits (43), Expect = 1415
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 CQPGFTG 8
C PGFTG
Sbjct: 520 CPPGFTG 526

Score = 21.0 bits (42), Expect = 1899
Identities = 7/11 (63%), Positives = 8/11 (72%)

Query: 1 KCQPGFTGARC 11
KC GFTG +C
Sbjct: 169 KCLTGFTGQKC 179

Score = 20.2 bits (40), Expect = 3419
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 CQPGFTG 8
CQ GFTG
Sbjct: 133 CQVGFTG 139

Score = 19.3 bits (38), Expect = 6156
Identities = 7/11 (63%), Positives = 8/11 (72%)

Query: 2 CQPGFTGARCT 12
C PG+ G RCT
Sbjct: 861 CAPGWQQRCT 871

Score = 19.3 bits (38), Expect = 6156
Identities = 6/12 (50%), Positives = 9/12 (75%)

Query: 2 CQPGFTGARCTE 13
C PG+ GA C++
Sbjct: 595 CNPGYMGAIKSD 606

Score = 19.3 bits (38), Expect = 6156
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
C P +TG CTE+V
Sbjct: 286 CPPQWTGQFCTEDV 299

gi|17136484|ref|NP_476729.1| slit CG8355-PB [Drosophila melanogaster]
gi|21645372|gb|AAM70966.1| CG8355-PB [Drosophila melanogaster]
Length = 1469

Score = 28.6 bits (60), Expect = 9.6
Identities = 9/12 (75%), Positives = 10/12 (83%), Gaps = 2/12 (16%)

Query: 2 CQ--PGFTGARC 11
CQ PG+TGARC
Sbjct: 971 CQCAPGYTGARC 982

Score = 25.2 bits (52), Expect = 100
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
CQ GF G CT+N+

Sbjct: 1052 CQAGFHGTNCTDNI 1065

Score = 23.1 bits (47), Expect = 437
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 2 CQPGFTG 8
CQPGF+G
Sbjct: 1012 CQPGFSG 1018

Score = 20.6 bits (41), Expect = 2548
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PG+TG C
Sbjct: 1139 CHPGYTGKWC 1148

Score = 17.6 bits (34), Expect = 19953
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 CQPGF 6
CQPG+
Sbjct: 934 CQPGY 938

>gi|103392|pir|B36665 slit protein 2 precursor - fruit fly (*Drosophila melanogaster*)
Length = 1469

Score = 28.6 bits (60), Expect = 9.6
Identities = 9/12 (75%), Positives = 10/12 (83%), Gaps = 2/12 (16%)

Query: 2 CQ--PGFTGARC 11
CQ PG+TGARC
Sbjct: 971 CQCAPGYTGARC 982

Score = 25.2 bits (52), Expect = 100
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 CQPGFTGARCTENV 15
CQ GF G CT+N+
Sbjct: 1052 CQAGFHGTNCTDNI 1065

Score = 23.1 bits (47), Expect = 437
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 2 CQPGFTG 8
CQPGF+G
Sbjct: 1012 CQPGFSG 1018

Score = 20.6 bits (41), Expect = 2548
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 2 CQPGFTGARC 11
C PG+TG C
Sbjct: 1139 CHPGYTGKWC 1148

Score = 17.6 bits (34), Expect = 19953
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 CQPGF 6

CQPG+
Sbjct: 934 CQPGY 938

gi|6755785|ref|NP_035717.1| tyrosine kinase receptor 1; D430008P04Rik [Mus musc
gi|1351248|sp|Q06806|TIE1 MOUSE Tyrosine-protein kinase receptor Tie-1 precursor
gi|543313|pir|JN0711 protein-tyrosine kinase (EC 2.7.1.112), receptor type tie pre
- mouse
gi|402602|emb|CAA52148.1| TIE receptor tyrosine kinase [Mus musculus]
gi|520946|emb|CAA56739.1| TIE1 [Mus musculus]
Length = 1134

Score = 28.6 bits (60), Expect = 9.6
Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 2 CQPGFTGARC 11
C PGFTG RC
Sbjct: 244 CPPGFTGTRC 253

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: May 29, 2003 2:04 AM
Number of letters in database: 462,300,935
Number of sequences in database: 1,438,044

Lambda	K	H
0.348	0.282	1.87

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Hits to DB: 26,193,600
Number of Sequences: 1438044
Number of extensions: 536775
Number of successful extensions: 12541
Number of sequences better than 20000.0: 100
Number of HSP's better than 20000.0 without gapping: 11086
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 12540
length of query: 23
length of database: 462,300,935
effective HSP length: 14
effective length of query: 9
effective length of database: 442,168,319
effective search space: 3979514871
effective search space used: 3979514871
T: 11
A: 40
X1: 14 (7.0 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 34 (18.9 bits)
S2: 34 (17.6 bits)